

(19)



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11)

EP 0 803 571 A2

(12)

EUROPEAN PATENT APPLICATION

(43) Date of publication:
29.10.1997 Bulletin 1997/44

(51) Int Cl.⁶: **C12N 15/12, C12N 15/62,**
C12Q 1/48

(21) Application number: **97302808.7**

(22) Date of filing: **24.04.1997**

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC
NL PT SE

(30) Priority: **24.04.1996 JP 126282/96**
28.10.1996 JP 300856/96
20.11.1996 US 752891

(71) Applicant: **Ueno, Naoto**
Sapporo-shi, Hokkaido 065 (JP)

(72) Inventors:
• **Matsumoto, Kunihiro**
Chikusa-ku, Nagoya-shi, Aichi (JP)

• **Nishida, Eisuke, Pakuhaimu Takaragaike 610**
Sakyo-ku, Kyoto-shi, Kyoto (JP)

(74) Representative: **Wakerley, Helen Rachael**
Reddle & Grose,
16 Theobalds Road
London WC1X 8PL (GB)

Remarks:

The applicant has subsequently filed a sequence listing and declared, that it includes no new matter.

(54) **Tab1 protein & dna coding therefor**

(57) DNA coding for TAB1 protein having activity which activates factor TAK1 in the TGF- β signaling path-

way, and having the amino acid sequence shown in Fig. 1.

EP 0 803 571 A2

Description

BACKGROUND OF INVENTION

1. Field of Invention

The present invention relates to a gene coding for TAB1 protein which forms a part of the signal-transduction pathway of Transforming Growth Factor- β (TGF β).

2. Related Art

TGF- β is a multifunctional factor which regulates various cellular functions. As one of those functions, TGF- β is responsible for the repair and reproduction of tissues with various types of injury.

Abnormal production of TGF- β in cases of chronic injury sometimes results in an imbalance between the repair and the reproduction of tissues and thus pathological fibrosis. Hepatic fibrosis is known as one condition resulting from an imbalance in TGF- β production. In the liver, TGF- β accelerates production of extracellular matrix proteins which are responsible for fibrosis, while inhibiting synthesis of extracellular matrix protein catabolic enzymes and inducing catabolic enzyme inhibitors, and it thus acts as a major causative factor of hepatic fibrosis.

One of known members of signal-transduction pathway belonging to the TGF- β superfamily is the Mitogen-Activated Protein Kinase Kinase Kinase (MAPKKK) system.

The MAPK pathway is a conserved eukaryotic signal-transduction pathway which converts receptor signals into various functions, and the system comprises 3 different protein kinases, specifically MAPKKK mentioned above, MAPKK and MAPK, with MAPK being activated through phosphorylation by MAPKK, and MAPKK in turn being activated by MAPKKK (E. Nishida et al., Trends Biochem. Sci. Vol.18, p.128 (1993); K.J. Blumer et al, op. cit. Vol.19, p.236 (1994); R.J. David, op. cit. Vol.19, p.470 (1994); C.J. Marshall, Cell, Vol.80, p.179 (1995)).

TAK1, which is a member of the MAPKKK family which functions in signal-transduction pathways belonging to the TGF- β superfamily, has been identified by K. Yamaguchi (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)).

TGF- β transduces signal through a heteromeric complex of type I and type II TGF- β receptors, which are transmembrane proteins comprising cytoplasmic serine- and threonine-specific kinase domains (J.L. Wrana et al., Nature, Vol.370, p.341 (1994); D.M. Kingsley et al., Genes Dev., Vol.8, p.133 (1994)). However, little is known at the molecular level about the signal-transduction mechanism downstream from the TGF- β receptors, and a gene coding for TAB1 protein has not yet been cloned.

SUMMARY OF INVENTION

The present invention can provide an isolated DNA coding for TAB1 protein which is a newly discovered member in the TGF- β receptor signal-transduction pathway, and to a gene coding therefor. The present invention further provides a screening method for TGF- β signal-transduction pathway inhibitors. TAB1 refers to a protein which binds to TAK1 (TAK1 Binding protein).

The present invention provides an isolated DNA coding for TAB1 protein having the amino acid sequence shown in SEQ ID NO: 1; an isolated DNA coding for a protein having an amino acid sequence shown in SEQ ID NO: 1 modified by substitution, deletion and/or addition of one or more amino acids in the amino acid sequence shown in SEQ ID NO: 1, and having a biological property of TAB1 protein; a protein wherein the 52nd amino acid of the amino acid sequence shown in SEQ ID NO: 1 is arginine; a DNA which can hybridize with DNA having the nucleotide sequence shown in SEQ ID NO: 1 under hybridization conditions of 60°C, 0.1 x SSC, 0.1% sodium dodecyl sulfate, and which has a biological property of TAB1 protein; a protein having an amino acid sequence consisting of amino acids from amino acid positions 21 to 579 of the amino acid sequence shown in SEQ ID NO: 1; and an isolated DNA coding a polypeptide having the amino acid sequence consisting of the 68 amino acids from amino acid positions 437 to 504 of the amino acid sequence shown in SEQ ID NO: 1.

The present invention further provides a method for producing any of the above-mentioned proteins or polypeptides comprising the steps of culturing a host transformed by an expression vector comprising DNA encoding the protein or polypeptide, and recovering the protein or polypeptide from the culture.

The present invention still further provides a method for inducing mammalian cells to produce any of the above-mentioned proteins or polypeptides comprising the step of introducing DNA encoding the protein or polypeptide into mammalian cells.

The present invention still further provides an expression vector comprising the DNA, and a host transformed by the expression vector.

The present invention still further provides a method for screening TGF- β signal-transduction pathway inhibitors.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the regions on the TAK1 protein to which TAB1 protein binds. The shaded areas indicate the TAK1 catalytic domain.

Fig. 2 shows complementation of the Stell deletion by the copresence of TAK1 and TAB1 in an Stell deletion strain, in the pheromone-activated MAPK pathway of yeast.

Fig. 3 is the results of electrophoresis shown in a photograph showing the results of the *in vitro* experiment indicating reinforcement of TAK1 activity by TAB1.

Fig. 4 shows the amino acid sequence of TAB1 with an insertion of partial TAK1 sequence for comparison.

Fig. 5 is an electrophoresis diagram showing expression of mRNA coding for TAB1 in various organs and tissues.

Fig. 6 is an immunoblot diagram showing association of TAB1 and TAK1 in mammalian cells.

Fig. 7 contains a graph showing enhancement of TAK1 kinase activity by TAB1 in mammalian cells (top), and a blot diagram showing comparable amounts of production of TAK1 and KN-MPK2.

Fig. 8 is a graph showing enhanced expression of a luciferase reporter gene by the copresence of TAK1 and TAB1 in mammalian cells stimulated by TGF- β .

Fig. 9 is a graph showing inhibition of the TGF- β -induced luciferase reporter gene expression by TAB1 lacking the C-terminus (TAB1 (1-418)).

DETAILED DESCRIPTION

The TAB1 protein encoded by DNA according to the invention has the characteristic of activating TAK1 by binding TAK1 in the signal-transduction pathway of transforming growth factor- β (TGF- β). This and other characteristics are described in detail Examples 2 to 4 and 6 to 10.

The TAB1 protein encoded by DNA of the invention has the amino acid sequence (SEQ ID NO: 1) derived from the nucleotide sequence of cDNA cloned by the method described in Examples 1 and 5. However, it is well known that proteins with biological activity exist whose amino acid sequences have been modified by a substitution, deletion and/or addition of one or more amino acids, and which maintain a biological property of the wild protein. Thus, the present invention encompasses DNA coding for proteins having an amino acid sequence modified by a substitution, deletion and/or addition of one or more amino acids in the amino acid sequence shown in SEQ ID NO: 1, and having a biological property of TAB1 protein.

One embodiment thereof is a protein wherein the 52nd amino acid of the amino acid sequence shown in SEQ ID NO: 1 is arginine.

It is also known that once DNA coding for a specific protein has been cloned, the DNA may be used as a probe for screening of a DNA library from organs or tissue different from the organs or tissue from which the protein was obtained, or a DNA library from another species, to obtain DNA coding for a protein with similar biological property though having a different amino acid sequence. Thus, the present invention also encompasses proteins encoded by DNA which can hybridize with DNA having the nucleotide sequence shown in SEQ ID NO: 1 under hybridization conditions of 60°C, 0.1 x SSC, 0.1% sodium dodecyl sulfate, and which has a biological property of TAB1 protein.

An example of a modified protein encoded by DNA according to the invention is a protein having an amino acid sequence consisting of amino acids from amino acid positions 21 to 579 of the amino acid sequence shown in SEQ ID NO: 1. This protein has the biological property of TAB1 protein. An instance of a modified polypeptide according to the invention is a polypeptide having the amino acid sequence consisting of the 68 amino acids from amino acid positions 437 to 504 of the amino acid sequence shown in SEQ ID NO: 1. This polypeptide has the properties of activating TAK1 kinase activity upon binding to TAK1.

Another example of a modified protein encoded by DNA according to the invention is a fused protein between the aforementioned protein or polypeptide and another protein, which has a biological activity of TAB1.

Proteins or polypeptides encoded by DNA of the invention can imitate the actual physiological function of TGF- β by, for example, activating TAK1 which is important to the TGF- β signal-transduction pathway, as well as inhibit binding between TAK1 and TAB1 by their binding to TAK1, and they are therefore useful for methods of screening substances which act as agonists or antagonists against cell growth suppression, immunosuppression and bone differentiation.

DNA coding for a protein of the invention is, for example, DNA coding for the amino acid sequence shown in SEQ ID NO: 1. Such DNA may be obtained, for example, by the method described in Examples 1 and 5, and it has the nucleotide sequence shown in SEQ ID NO: 1. However, DNA coding for the amino acid sequence shown in SEQ ID NO: 1 does not necessarily have the nucleotide sequence shown in SEQ ID NO: 1, as it may consist of other codons coding for the same amino acids. For example, the human derived nucleotide sequence shown in SEQ ID NO: 1 may be altered to include a codon which is efficiently translated in such microorganisms as bacteria or yeast, and this may be accomplished using a well-known technique such as site-specific mutagenesis with a primer.

DNA according to the invention coding for a protein or polypeptide having an amino acid sequence modified by a

substitution, deletion and/or addition of one or more amino acids in the amino acid sequence shown in SEQ ID NO: 1 may be prepared by a well-known method such as site-specific mutagenesis or the PCR, using DNA with the nucleotide sequence shown in SEQ ID NO: 1 as the template. Alternatively, DNA coding for a protein or polypeptide wherein the modified amino acid sequence is shorter than the natural protein may be obtained, for example, by introducing a translation initiation codon and/or translation termination codon into naturally occurring DNA, such as cDNA. The introduction of these codons may be accomplished by site-specific mutagenesis or the PCR. Alternatively, it may be achieved by cleaving the natural DNA, such as cDNA, with an appropriate restriction enzyme, and adding the desired oligonucleotide if necessary.

DNA which can be hybridized with DNA having the nucleotide sequence shown in SEQ ID NO: 1 of the invention and which codes for a protein having a biological property of TAB1 may be obtained by screening a genomic DNA library or cDNA library prepared, for example, from the various tissues and organs mentioned in Example 6, including the heart, brain, placenta, liver, skeletal muscle, kidney, pancreas, spleen, thymus, prostate, testicles, ovaries, small intestine, colon, peripheral leukocytes, etc., using the nucleotide sequence shown in SEQ ID NO: 1 of the invention or a portion thereof as the probe. The DNA library is not limited to a human derived one, and may be derived from other animals such as rats, mice, rabbits, goats, sheep, cattle or pigs.

The present invention also relates to an expression vector comprising an aforementioned DNA and to a host transformed therewith. The expression vector will differ depending on the host. The host cells used according to the invention may be from any prokaryotic or eukaryotic organisms. The prokaryotic organisms used may be bacteria, for example, microorganisms belonging to the genus *Escherichia coli*, microorganisms belonging to the genus *Bacillus* such as *Bacillus subtilis*, etc., and the eukaryotic organisms may be lower eukaryotic organisms, such as filamentous fungi and yeast.

Filamentous fungi include microorganisms belonging to the genus *Aspergillus* such as *Aspergillus niger* and *Aspergillus oryzae* and microorganisms belonging to the genus *Penicillium*, while the yeast may be microorganisms belonging to the genus *Saccharomyces* such as *Saccharomyces cerevisiae*.

Higher eukaryotic organisms which may be used include various animal and plant cells, for example, immortalized cultured animal cells such as COS cells, CHO cells and NIH3T3, etc. Insect cells such as Sf9, Sf12, etc. may also be used.

The expression vector of the invention includes, in addition to DNA coding for a protein or polypeptide of the invention, expression regulating sequences, such as promoters, which are functionable in the host.

Promoters for bacteria, for example *E. coli*, include T3 and T7, while promoters for yeast include glycolytic enzyme gene promoters such as GAL1 promoter and GAL4 promoter. The promoter for animal cells may be a viral promoter, such as CMV promoter or SV40 promoter.

The transformation of the host by an expression vector, culturing the host, and the collection and purification of the protein or polypeptide of the invention from the culture may be accomplished according to conventional methods. For example, the isolation and purification of the protein or polypeptide from the culture may be accomplished using any conventional means for isolating and purifying proteins and polypeptides, such as ammonium sulfate precipitation, gel filtration or reverse phase HPLC, either alone or in combinations.

The present invention also relates to a screening method for TGF- β signal-transduction pathway inhibitors. A sample containing TGF- β signal-transduction pathway inhibitors is brought to contact with or introduced into cells expressing a protein with a biological activity TAB1 and TAK1 (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)), and the TAK1 activity is then measured. The protein or polypeptide with biological activity of TAB1 and TAK1 may also be fused with another protein, and the cells expressing them may be yeast cells or mammalian cells. This screening system may be constructed according to the method described in Examples 1, 2, 3, 4, 7, 8 and 9.

The sample containing TGF- β signal-transduction pathway inhibitors is brought to contact with or introduced into the constructed screening system, and the TAK1 kinase activity is measured. The method for measuring the TAK1 kinase activity may be measurement of the kinase activity of TAK1 itself, or measurement of the kinase activity of MAPKK or MAPK which are downstream from TAK1 in the signal-transduction pathway and are activated by TAK1. The activity of a target gene in the MAPK pathway or a reporter gene under the control of the target gene promoter may also be measured based on the amount of mRNA or expressed form of the gene.

The screening method for TGF- β signal-transduction pathway inhibitors according to the invention allows screening of substances which inhibit binding between TAB1 and TAK1 and can thus serve as a means of therapy for diseases involving abnormal production of TGF- β .

EXAMPLES

The present invention will now be explained in more detail by way of the following examples.

Example 1

Analysis of the TAK1-dependent pathway functioning for TGF- β signal-transduction was made using a yeast 2-hybrid system (S. Fields et al., *Trend Genet.* 10, 286 (1994)), and a protein having direct interaction with TAK1 was sought.

First, an expression vector was constructed by linking the TAK1 gene and a gene coding for the LexA DNA-binding domain. pLexA-TAK1 Δ contains the TAK1 Δ N coding sequence (K. Yamaguchi et al., *Science*, Vol.270, p.2008 (1995)) inserted in frame into pBTM116 (A.B. Vojtek et al., *Cell*, Vol.74, p.205 (1993)). A yeast 2-hybrid system was used to identify a protein encoded in a human brain cDNA library and interacting with TAK1 Δ N.

The two hybrids were expressed in *Saccharomyces cerevisiae* L40 (LYS2:LexA-HIS3) containing an integrated reporter construct with a binding site for LexA protein located upstream from the yeast HIS3 coding region. Interaction between the two hybrid proteins causes transactivation of the reporter construct, allowing growth of the yeast in the absence of histidine (SC-His).

The LexA-TAK1 Δ N fused protein alone confers expression of HIS3 in a sufficient amount to allow growth without requiring exogenous histidine. However, histidine auxotrophy can be achieved by growing the cells in the presence of 40 mM 3-aminotriazole (3-AT) which is a chemical inhibitor of the HIS3 gene product imidazole glycerol dehydrogenase (G.M. Kishore et al., *Annu. Rev. Biochem.* Vol.57, p.627 (1988)).

Yeast was transformed using a bait plasmid together with a fish plasmid containing the human brain cDNA expression library clone linked to the gene coding for the GAL4 activating domain (GAD). A positive clone of TAB1 cDNA coding for the protein was obtained from about 1×10^6 transformants. The GAD fused protein expressed by this isolated DNA will hereinafter be referred to as GAD-TAB1.

Example 2

A series of LexA-TAK1 deletion chimera were tested by the 2-hybrid method to determine the site in TAK1 which is responsible for interaction with TAB1. An expression vector coding for the full TAK1 or deletion construct thereof fused to the LexA DNA-binding domain was used for simultaneous transformation of the yeast reporter strain L40 together with pGAD-TAB1. The DNA coding for each of the TAK1 deletion constructs was prepared from DNA coding for the full TAK1.

The aforementioned plasmid pGAD-TAB1 was obtained by cloning TAB1 cDNA at the EcoRI site of pBS (W.O. Bullock et al., *Biotechniques*, Vol.5, p.376 (1987)). The interaction between the fused proteins expressed by this plasmid is indicated by the ability of the yeast strain to grow on a plate of SC-HIS medium containing 40 mM 3-AT. The results are shown in Fig. 1. The right side of this graph indicates whether TAK1 or its deletion form interacted with TAB1 (+) or not (-). These results demonstrate that TAB1 interacts with the N-terminal domain of TAK1.

Example 3

A protein interacting with TAK1 may contain both the upstream control region and the downstream target. If TAB1 plays a role in activation of TAK1, then their simultaneous expression would be expected to influence activity of TAK1 in yeast. The present inventors have disclosed a system for assaying mammalian MAPKKK activity in a yeast pheromone-induced MAPK pathway (K. Yamaguchi et al., *Science*, Vol.270, p.2008 (1995); K. Irie et al., *Science*, Vol.265, p.1716 (1994)). An activated form of TAK1 (TAK1 Δ N) can substitute for Ste11 MAPKKK activity.

Specifically, the pheromone-activated MAPK pathway consists of Ste11, Ste7, and Fus3 or Kss1 kinases, which correspond to MAPKKK, MAPKK and MAPK, respectively. These yeast protein kinases act sequentially to transduce signals to the transcription factor Ste12, upon which Ste12 in turn activates transcription of mating-specific genes such as FUS1 (I. Herskowitz, *Cell*, Vol.80, p.187 (1995); D.E. Levin et al., *Curr. Opin. Cell Biol.*, Vol.7, p.197 (1995); J. Schultz et al., Jr. *Curr. Opin. Gene Dev.*, No.5, p.31 (1995)).

The FUS1p::HIS3 reporter gene comprises the FUS1 upstream activating sequence linked to the HIS3 open reading frame, and signal activity of the his3 Δ FUS1p::HIS3 strain may be monitored by the ability of cells to grow on SC-His medium (His⁻ phenotype).

Strain his3 Δ ste11FUS1p::HIS3STE7^{P368} (proline substitution at serine-368) has a His⁻ phenotype (K. Irie et al., *Science*, Vol.265, p.1716 (1994)).

Expression of TAK1 Δ N in this strain confers a His⁺ phenotype (K. Yamaguchi et al., *Science*, Vol.270, p.2008 (1995)). Thus, the activated form of TAK1 may substitute for Ste11 activity in an Ste7^{P368}-dependent manner. However, expression of the full-length TAK1 does not complement the ste11 Δ mutation, suggesting that the yeast does not have the putative activating factor for TAK1 (K. Yamaguchi et al., *Science*, Vol.270, p.2008 (1995)).

The GAD-TAB1 constructs were tested for their ability to complement the ste11 Δ mutation in the presence of TAK1, using the yeast MAPK pathway. Specifically, yeast strain Sy1984-P (his3 Δ ste11FUS1p::HIS3STE7^{P368}) was transformed with pNV11-HU11 (TAK1 Δ N) + pGAD10 (GAD) (Clontech), pNV11-HU11F (TAK1) + pGAD10, pNV11-HU11F

+ pGAD-TAB1 or pNV11 + pGAD-TAB, and the transformants were folded onto an SC-His plate and incubated at 30°C.

The aforementioned strain Sy1984-P is Sy1984 (his3 Δ ste11FUS1p::HIS3) transformed by plasmid pNC318-p368 containing STE7^{P368} under the control of CYC1 promoter (K. Irie et al., Science, Vol.265, p.1716 (1994)). The aforementioned plasmids pNV11-HU11 and pNV11-HU11F respectively express the shortened TAK1 Δ AN (amino acids 21-579) and the full-length TAK1 under the control of TDH3 promoter (K. Yamaguchi et al, Science, Vol.270, p.2008 (1995)).

The results are shown in Fig. 2. The left panel indicates whether the yeast strain tested expressed TAK1 Δ AN or TAK1, and whether GAD-TAB1 was simultaneously expressed or not. The right panel shows the growth of the cells on the SC-His plate. Each of the patches represents the results for an independent transformant.

The GAD-TAB1 and TAK1 simultaneous transformant restored the effect of the Ste11 deletion. This indicates that TAB1 reinforces the function of TAK1.

Example 4

In order to determine whether TAK1 activity is increased in TAB1-expressing yeast, an expression DNA vector containing TAK1 carrying the hemagglutinin (HA)-derived C-terminal epitope and a catalytically inactive TAK1 mutant [TAK1-K63W wherein lysine at position 63 of the ATP-binding site is replaced with tryptophan (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995))] was used to transform yeast cells in the absence and in the presence of the TAB1 gene.

The DNA sequence coding for an epitope recognized by the HA-specific monoclonal antibody 12CA5 was joined in frame with the TAK1-coding sequence and TAK1-K63W C-terminus by the polymerase chain reaction (PCR). All of the constructs were expressed by TDH promoter. The TAB1 expression plasmid pGAP-HTH9M expresses 68 C-terminal amino acids. YE pGAP112 is a multicopy plasmid TRP1 containing TDH3 promoter [H. Banno et al., Mol. Cell Biol. 13, 475 (1993)].

A sequence coding for the 68 C-terminal amino acids of TAB1 was amplified by the PCR using the 5' primer: 5'-GAGAATTCATGCGGCAAAGC-3' (SEQ ID NO: 2) containing the EcoRI site and ATG codon and the 3'-primer: 5'-GGGTCTGACTACGGTGC-3' (SEQ NO: 3) containing the Sall site. A 240 bp EcoRI-Sall fragment produced by PCR was inserted into the EcoRI-Sall gap of YE pGAP112 to construct pGAD-HTH9M.

The results are shown in Fig. 3. As described above, yeast strain Sy1984 was transformed with the aforementioned plasmid coding for TAK1-HA and plasmid coding for TAK1-K63W, and the empty vector YE pGAP112(-) or pGAP-HTH9M(+) coding for TAB1 was additionally inserted into the transformant. TAK1-HA(-) or TAK1-K63W-HA(KN) was immunoprecipitated from each of the cell extracts and the immunoprecipitates were subjected to *in vitro* kinase assays. Specifically, 60 ml of yeast cell culture was allowed to grow to an optical density of 0.8 at 600 nm, and a cell extract was prepared with a cytolytic buffer solution (K. Irie et al., Science, Vol.265, p.1716 (1994)) and then separated by centrifugation at 100,000 g for 30 minutes.

The supernatant was subjected to immunoprecipitation with an antibody against HA. That is, a portion (300 μ l) of the supernatant was mixed with 2 μ l of antibody and 90 μ l of Protein A-Sepharose, and the immunocomplex was washed 3 times with a cytolytic buffer solution and used for the kinase assay (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)). Immunoblot analysis of each immunoprecipitate with the HA-specific monoclonal antibody 12CA5 demonstrated that approximately the same amount of TAK1-HA or TAK1-K63W-HA was recovered in each sample. This suggests that expression of TAB1 does not affect the amount of TAK1 expression.

The immunoprecipitated TAK1 was assayed based on the ability to activate recombinant XMEK2 (SEK1), with the recombinant XMEK2 (SEK1) activity being assayed based on its ability to phosphorylate catalytically inactive (KN)p38 (MPK2) (K. Yamaguchi et al., Science, No.270, p.2008 (1995)). After electrophoresis, phosphorylation of KN-p38 (MPK2) was detected by autoradiography. No extract exhibited a kinase assay value without the enzyme extract. This level corresponds to the XMEK2 basal activity. The experiment was conducted at least 3 times, giving the same results each time.

The results are shown in Fig. 3. The results of kinase assay for TAK1-HA and TAK1-K36W-TAK1 indicate that TAB1 increases TAK1 kinase activity. The activity increase was not observed for immunocomplexes from cells expressing TAK1-K63WKN and TAB1, indicating that the observed kinase activity was attributable to TAK1. These results demonstrate that TAB1 activates TAK1 kinase activity by directly binding to the catalytic domain of TAK1.

Example 5

To obtain the full-length coding sequence for TAB1, a human kidney library was screened using as a probe the aforementioned partial sequence of TAB1 cDNA obtained from the yeast 2-hybrid system. Two independent clones carried 3.1 kb cDNA containing a single open reading frame (ORF) starting from the initial methionine codon matching the Kozak consensus. The 5'-terminus was identified by the 5' RACE method using 5'-RACE-Ready cDNA (Clontech).

The proposed N-terminal nucleotide sequence of the coding sequence (CCAAATGG) corresponds to the Kozak consensus (M. Kozak, J. Cell Biol. Vol.108, p.229 (1989)), and the ATG codon is not present before it.

The TAB1 nucleotide sequence was determined by the dideoxynucleotide chain termination method. An amino acid sequence was deduced from the nucleotide sequence of the full-length TAB1 cDNA. As a result, two different clones were obtained with cytosine and adenine as the 185th nucleotide, respectively. The clone with cytosine as the 185th nucleotide encodes for serine as the 52nd amino acid, and the clone with adenine as the 185th nucleotide encodes arginine as the 52nd amino acid.

The nucleotide sequence of the clone with cytosine as the 185th nucleotide is shown in SEQ NO: 1, and its amino acid sequence is shown in Fig. 4 and in SEQ ID NO: 1. The nucleotide sequence of the clone with adenine as the 185th nucleotide is shown in SEQ ID NO: 4, and its amino acid sequence is also shown in SEQ ID NO: 4.

The cDNA of the clone with cytosine as the 185th nucleotide was subcloned at the EcoRI and SmaI sites of pBS to prepare plasmid TAB1-f-4, while the cDNA of the clone with adenine as the 185th nucleotide was subcloned at the EcoRI site of pBS to prepare plasmid pBS-TAB1. *E. coli* containing plasmid pBS-TAB1 was named *Escherichia coli* HB101 (pBS-TAB1) and was deposited at the National Institute of Bioscience and Human Technology Agency of Industrial Science and Technology on April 19, 1996 as FERM BP-5508. *E. coli* containing plasmid TAB1-f-4 was named *Escherichia coli* DH5 α (TAB1-f-4) and was deposited at the National Institute of Bioscience and Human Technology Agency of Industrial Science and Technology on July 19, 1996 as FERM BP-5599.

The following experiment was conducted using the clone having the nucleotide sequence shown in SEQ ID NO: 1. In Fig. 4, A = Ala, C = Cys, D = Asp, E = Glu, F = Phe, G = Gly, H = His, I = Ile, K = Lys, L = Leu, M = Met, N = Asn, P = Pro, Q = Gln, R = Arg, S = Ser, T = Thr, V = Val, W = Trp and Y = Tyr. The 68 C-terminal amino acids of GAD-TAB1 isolated using the yeast 2-hybrid system are boxed.

The N-terminal sequence of TAK1 is aligned to show the region with similarity to the same segment of TAK1. The identical and conserved amino acids with respect to those of TAK1 are marked with asterisks and dots, respectively.

The ORF suggested a protein of 504 amino acids having a molecular size of 55 kDa, without clear similarity to any known protein and without any motif indicating biological function.

Example 6

The expression patterns of TAB1 mRNA in different human cells were analyzed by Northern blotting. Human tissue blots (Clontech) of mRNA isolated from 18 tissues were probed with ³²P-labelled TAB1 cDNA, and subjected to autoradiography. The results are shown in Fig. 5. Each of the lanes contained 2 μ g of mRNA. The probe was labelled with [α -³²P]-dCTP using a Multiprime Labeling Kit (Amersham), and hybridized as described by H. Shibuya et al., Nature, Vol.357, p.700 (1992). A major transcription product of about 3.5 kb was detected in all of the tissues tested.

Example 7

In order to confirm association of TAB1 and TAK1 in mammalian cells, an expression vector producing HA epitope-labelled TAK1 (HA-TAK1) (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)) and an expression vector producing Myc epitope-labelled TAB1 (Myc-TAB1) were used for transient transfection of MC3T3-E1 murine osteoblasts (S. Ohta et al., FEBS Lett., Vol.314, p.356 (1992)). The latter plasmid was obtained in the following manner.

The full-length TAB1 cDNA was subcloned in pCS2MT vector containing 6 copies of the Myc epitope (LEQKLI-SEEDLN) (single letter amino acid sequence notation) recognized by the Myc-specific monoclonal antibody 9E10 (D. L. Turner et al., Genes Dev., Vol.8, p.1434 (1994)). In the plasmid thus obtained, pCS2MT-TAB1, the Myc epitope tag is linked in frame with the DNA sequence corresponding to the N-terminus of TAB1. pCS2MT-TAB1 was digested with BamHI and XbaI. The fragment was isolated and inserted at the EcoRI-XbaI site of the mammalian expression vector pEF. This plasmid causes expression of TAB1 from the human elongation factor 1 α (EF1 α) promoter.

The cell extract was subjected to immunoprecipitation with the HA-specific monoclonal antibody 12CA5 (lane 2 in Fig. 6), the Myc-specific monoclonal antibody 9E10 (lane 3 in Fig. 6) or a control nonimmune IgG (lane 4 in Fig. 6). The immunocomplex was washed and separated by SDS-PAGE, and then transferred to nitrocellulose for immunoblotting using the Myc-specific antibody (top lanes of Fig. 6) and HA-specific antibody (bottom lanes of Fig. 6).

The cell extracts were then immediately subjected to immunoblot analysis (lane 1 of Fig. 6). As Fig. 6 shows, a considerable amount of Myc-TAB1 was detected in each immunoprecipitation, indicating that TAK1 can be immunoprecipitated with TAB1. A reciprocal experiment blotting the immunoprecipitated protein with the HA-specific antibody confirmed association of TAB1 and TAK1. These experiments indicate that TAB1 can associate with TAK1 in mammalian cells as in yeast.

Example 8

It was investigated whether overexpression of TAB1 can activate TAK1 kinase activity. MC3T3-E1 cells were transiently transfected with HA-TAK1 in the presence of (+) and in the absence of (-) Myc-TAB1. The cells were treated (+) or untreated (-) with 20 ng/ml TGF- β 1 for 10 minutes and then HA-TAK1 was immunoprecipitated in the manner described in Example 3, after which the kinase activity was assayed. Specifically, a portion of the immunoprecipitate was immunoblotted with HA-specific antibody. The results are shown in Fig. 7.

The activity is given as a fold increase relative to the amount of HA-TAK1 from unstimulated cells, and is expressed as mean \pm SEM from at least 3 experiments (top graph in Fig. 7). HA-TAK1 did not directly phosphorylate KH-p38 (MPK2) (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)). The middle panel is the autoradiogram showing phosphorylation of KN-p38(MPK2). The lower panel shows immunoblot analysis of each of the immunoprecipitates with the HA-specific monoclonal antibody 12CA5, where it is seen that approximately the same amount of TAK-HA was recovered in each sample. The data shown in the middle and lower panels are from typical experiments.

The *in vitro* assay of the TAK1 immunoprecipitation suggests that TAK1 activity was stimulated in cells transfected with TAB1 even in the absence of TGF- β . Activation of TAK1 by overexpression of TAB1 was comparable to the activation observed in cells stimulated with TGF- β which expressed only HA-TAK1.

Example 9

TGF- β causes rapid increase in the amount of mRNA coding for plasminogen activating factor inhibitor-1 (PAI-1) (M.R. Keeton et al., J. Biol. Chem., Vol.266, p.23048 (1991)). Overexpression of the activated form of TAK1 (TAK1 Δ N) results in constitutive activation of a reporter gene containing the luciferase gene under the control of the TGF- β -inducible PAI-1 gene promoter (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)). We investigated whether overexpression of TAB1 leads to activation of the luciferase reporter gene.

Mv1Lu cells were transiently transfected by the calcium phosphate method (H. Shibuya et al., Nature, Vol.357, p.700 (1992)) using a reporter plasmid p800neoLUC (M. Abe et al., Analyt. Biochem., Vol.216, p.276 (1994)) and the TAB1-expressing plasmid pEF-TAB1 or TAK1-encoding expression plasmid (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)). Plasmid pEF-TAB1 contains the full-length TAB1 coding sequence under the control of EF1 α promoter, and was constructed by cleaving pEF with EcoRI and inserting the EcoRI fragment from plasmid TAB1-f-4.

The plasmid TAB1-f-4 was constructed by subcloning TAB1 cDNA at the EcoRI and SmaI sites of pBS. The cells were incubated for 20 hours with and without 30 ng/ml of human TGF- β 1, an extract was prepared, and the luciferase was assayed (H. Shibuya et al., Mol. Cell Biol., Vol.14, p.5812 (1994)). The luciferase activity was compensated based on expression of β -galactosidase.

Specifically, the transfection efficiency was compensated by simultaneous transfection with pXeX- β -Gal vector (A. D. Johnson et al., Gene, Vol.147, p.223 (1994)) in all of the luciferase reporter experiments. Measurement of β -galactosidase was made according to the instructions of the manufacturer (Clontech), using the cell lysate prepared for the luciferase measurement. The luciferase activity was given as the fold increase with respect to the activity of unstimulated cells transfected with the vector. All of the transfection and luciferase measurements were conducted at least 5 times, with triplicates of each experiment.

The results are shown in Fig. 8. Here, KN indicates the catalytically inactive TAK1-K63W. The data is expressed as the mean \pm SEM of the luciferase activity from triplicates in a representative experiment. Overexpression of both TAK1 and TAB1 induced expression of the reporter gene even in the absence of TGF- β , but overexpression of only TAK1 or TAB1 had virtually no effect on the constitutive amount of luciferase activity. These experimental results indicate that TAB1 reinforces TAK1 activity in mammalian cells.

Although overexpression of the TAK1-K63W mutant inhibited TGF- β -stimulated luciferase activity (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)), this is presumably due to sequestering of essential elements in the pathway. On the other hand, overexpression of TAB1 reduces the inhibiting effect of TAK1-K63W, suggesting the possibility that TAB1 is absorbed by overexpression of TAK1-K63W.

Example 10

The 68 C-terminal amino acids of TAB1 [TAB1 (437-504)] were sufficient to bind to and activate TAK1, suggesting that the N-terminal domain of TAB1 performs a regulatory role on the function of TAB1. To test this possibility, a shortened form of TAB1 lacking the C-terminal TAK1-binding domain [TAB1 (1-418)] was constructed. Mv1Lu cells were transiently transfected with p800nedUC reporter and an expression vector coding for TAB1 (1-418) or TAB1 (full-length) in the amounts shown in Fig. 9, and these were complemented with the pEF control vector.

The expression vector coding for TAB1 (1-418) was constructed in the following manner. The 1.3 kb EcoRI-HincII fragment of plasmid TAB1-f-4 (containing the TAB1 N-terminal region of amino acids 1-418) was subcloned in pKT10

vector to construct pKT10-TAB1 (1-418). pEF was cleaved with EcoRI and Sall, and the EcoRI-Sall fragment from pKS10-TAB1 (1-418) was inserted therein to construct pEF-TAB1 (1-418).

Next, the cells were incubated for 20 hours with and without 30 ng/ml of human TGF- β 1, and the cell lysate was measured for luciferase activity. The values were expressed as fold induction in terms of a percent with respect to the control cells transfected with pEF. No induction of luciferase with TGF- β (1-fold induction) corresponds to 0%. All of the transfection and luciferase measurements were conducted at least 3 times, and a series of 3 of each of the experiments were conducted. The data is expressed as the mean \pm SEM of the luciferase activities from triplicates in a representative experiment.

The results are shown in Fig. 9. Overexpression of TAB1 (1-418) in Mv1Lu cells suppressed activity of the reporter gene induced by TGF- β stimulation. Thus, TAB1 (1-418) acts as the dominant negative inhibitor on gene expression induced by TGF- β . These results indicate that TAB1 plays a role in TGF- β signaling.

The mechanism of induction of TAK1 activation by TAK1 is believed to be that TAB1 binding to TAK1 induces the necessary conformational changes for activation. Since removal of the 20 N-terminal amino acids of TAK1 causes constitutive activation of the protein kinase, this suggests that the N-terminal domain hinders the catalytic domain, thus inhibiting kinase activity (K. Yamaguchi et al., Science, Vol.270, p.2008 (1995)). TAB1 may eliminate the negative control domain of TAK1 from its catalytic domain. The C-terminus of TAB1 which functions as the TAK1-binding site contains a serine- and threonine-rich region similar to the region found at the N-terminus of TAK1. Therefore, TAB1 is probably an important signaling intermediate between TGF- β and TAK1 MAPKKK.

SEQUENCE LISTING

```

5      SEQ ID NO: 1
      Sequence length: 1560
      Sequence type: Nucleic acid
      Strandedness: Double
10     Topology: Linear
      Molecular type: cDNA
      Sequence
15     GAATTCGTGG CCCGCAGGGT TCCTCCAAG ATG GCG GCG CAG AGG AGG AGC TTG 53
                                         Met Ala Ala Gln Arg Arg Ser Leu
                                         5
      CTG CAG AGT GAG CAG CAG CCA AGC TGG ACA GAT GAC CTG CCT CTC TGC 101
      Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys
          10              15              20
      CAC CTC TCT GGG GTT GGC TCA GCC TCC AAC CGC AGC TAC TCT GCT GAT 149
      His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp
          25              30              35              40
      GGC AAG GGC ACT GAG AGC CAC CCG CCA GAG GAC AGC TGG CTC AAG TTC 197
      Gly Lys Gly Thr Glu Ser His Pro Pro Glu Asp Ser Trp Leu Lys Phe
          30              45              50              55
      AGG AGT GAG AAC AAC TGC TTC CTG TAT GGG GTC TTC AAC GGC TAT GAT 245
      Arg Ser Glu Asn Asn Cys Phe Leu Tyr Gly Val Phe Asn Gly Tyr Asp
          35              60              65              70
      GGC AAC CGA GTG ACC AAC TTC GTG GCC CAG CGG CTG TCC GCA GAG CTC 293
      Gly Asn Arg Val Thr Asn Phe Val Ala Gln Arg Leu Ser Ala Glu Leu
          40              75              80              85
      CTG CTG GGC CAG CTG AAT GCC GAG CAC GCC GAG GCC GAT GTG CGG CGT 341
      Leu Leu Gly Gln Leu Asn Ala Glu His Ala Glu Ala Asp Val Arg Arg
          45              90              95              100
      GTG CTG CTG CAG GCC TTC GAT GTG GTG GAG AGG AGC TTC CTG GAG TCC 389
      Val Leu Leu Gln Ala Phe Asp Val Val Glu Arg Ser Phe Leu Glu Ser
          50              105              110              115              120
      ATT GAC GAC GCC TTG GCT GAG AAG GCA AGC CTC CAG TCG CAA TTG CCA 437
      Ile Asp Asp Ala Leu Ala Glu Lys Ala Ser Leu Gln Ser Gln Leu Pro
          55              125              130              135

```

EP 0 803 571 A2

5 GAG GGA GTC CCT CAG CAC CAG CTG CCT CCT CAG TAT CAG AAG ATC CTT 485
 Glu Gly Val Pro Gln His Gln Leu Pro Pro Gln Tyr Gln Lys Ile Leu
 140 145 150
 GAG AGA CTC AAG ACG TTA GAG AGG GAA ATT TCG GGA GGG GCC ATG GCC 533
 Glu Arg Leu Lys Thr Leu Glu Arg Glu Ile Ser Gly Gly Ala Met Ala
 10 155 160 165
 GTT GTG GCG GTC CTT CTC AAC AAC AAG CTC TAC GTC GCC AAT GTC GGT 581
 Val Val Ala Val Leu Leu Asn Asn Lys Leu Tyr Val Ala Asn Val Gly
 170 175 180
 15 ACA AAC CGT GCA CTT TTA TGC AAA TCG ACA GTG GAT GGG TTG CAG GTG 629
 Thr Asn Arg Ala Leu Leu Cys Lys Ser Thr Val Asp Gly Leu Gln Val
 185 190 195 200
 20 ACA CAG CTG AAC GTG GAC CAC ACC ACA GAG AAC GAG GAT GAG CTC TTC 677
 Thr Gln Leu Asn Val Asp His Thr Thr Glu Asn Glu Asp Glu Leu Phe
 205 210 215
 25 CGT CTT TCG CAG CTG GGC TTG GAT GCT GGA AAG ATC AAG CAG GTG GGG 725
 Arg Leu Ser Gln Leu Gly Leu Asp Ala Gly Lys Ile Lys Gln Val Gly
 220 225 230
 30 ATC ATC TGT GGG CAG GAG AGC ACC CGG CGG ATC GGG GAT TAC AAG GTT 773
 Ile Ile Cys Gly Gln Glu Ser Thr Arg Arg Ile Gly Asp Tyr Lys Val
 235 240 245
 35 AAA TAT GGC TAC ACG GAC ATT GAC CTT CTC AGC GCT GCC AAG TCC AAA 821
 Lys Tyr Gly Tyr Thr Asp Ile Asp Leu Leu Ser Ala Ala Lys Ser Lys
 250 255 260
 40 CCA ATC ATC GCA GAG CCA GAA ATC CAT GGG GCA CAG CCG CTG GAT GGG 869
 Pro Ile Ile Ala Glu Pro Glu Ile His Gly Ala Gln Pro Leu Asp Gly
 265 270 275 280
 45 GTG ACG GGC TTC TTG GTG CTG ATG TCG GAG GGG TTG TAC AAG GCC CTA 917
 Val Thr Gly Phe Leu Val Leu Met Ser Glu Gly Leu Tyr Lys Ala Leu
 285 290 295
 GAG GCA GCC CAT GGG CCT GGG CAG GCC AAC CAG GAG ATT GCT GCG ATG 965
 Glu Ala Ala His Gly Pro Gly Gln Ala Asn Gln Glu Ile Ala Ala Met
 300 305 310
 50 ATT GAC ACT GAG TTT GCC AAG CAG ACC TCC CTG GAC GCA GTG GCC CAG 1013
 Ile Asp Thr Glu Phe Ala Lys Gln Thr Ser Leu Asp Ala Val Ala Gln
 315 320 325
 55

EP 0 803 571 A2

GCC GTC GTG GAC CGG GTG AAG CGC ATC CAC AGC GAC ACC TTC GCC AGT 1061
 Ala Val Val Asp Arg Val Lys Arg Ile His Ser Asp Thr Phe Ala Ser
 5 330 335 340
 GGT GGG GAG CGT GCC AGG TTC TGC CCC CGG CAC GAG GAC ATG ACC CTG 1109
 Gly Gly Glu Arg Ala Arg Phe Cys Pro Arg His Glu Asp Met Thr Leu
 10 345 350 355 360
 CTA GTG AGG AAC TTT GGC TAC CCG CTG GGC GAA ATG AGC CAG CCC ACA 1157
 Leu Val Arg Asn Phe Gly Tyr Pro Leu Gly Glu Met Ser Gln Pro Thr
 365 370 375
 15 CCG AGC CCA GCC CCA GCT GCA GGA GGA CGA GTG TAC CCT GTG TCT GTG 1205
 Pro Ser Pro Ala Pro Ala Ala Gly Gly Arg Val Tyr Pro Val Ser Val
 380 385 390
 20 CCA TAC TCC AGC GCC CAG AGC ACC AGC AAG ACC AGC GTG ACC CTC TCC 1253
 Pro Tyr Ser Ser Ala Gln Ser Thr Ser Lys Thr Ser Val Thr Leu Ser
 395 400 405
 25 CTT GTC ATG CCC TCC CAG GGC CAG ATG GTC AAC GGG GCT CAC AGT GCT 1301
 Leu Val Met Pro Ser Gln Gly Gln Met Val Asn Gly Ala His Ser Ala
 410 415 420
 TCC ACC CTG GAC GAA GCC ACC CCC ACC CTC ACC AAC CAA AGC CCG ACC 1349
 30 Ser Thr Leu Asp Glu Ala Thr Pro Thr Leu Thr Asn Gln Ser Pro Thr
 425 430 435 440
 TTA ACC CTG CAG TCC ACC AAC ACG CAC ACG CAG AGC AGC AGC TCC AGC 1397
 35 Leu Thr Leu Gln Ser Thr Asn Thr His Thr Gln Ser Ser Ser Ser
 445 450 455
 TCT GAC GGA GGC CTC TTC CGC TCC CGG CCC GCC CAC TCG CTC CCG CCT 1445
 Ser Asp Gly Gly Leu Phe Arg Ser Arg Pro Ala His Ser Leu Pro Pro
 40 460 465 470
 GGC GAG GAC GGT CGT GTT GAG CCC TAT GTG GAC TTT GCT GAG TTT TAC 1493
 Gly Glu Asp Gly Arg Val Glu Pro Tyr Val Asp Phe Ala Glu Phe Tyr
 475 480 485
 45 CGC CTC TGG AGC GTG GAC CAT GGC GAG CAG AGC GTG GTG ACA GCA CCG 1541
 Arg Leu Trp Ser Val Asp His Gly Glu Gln Ser Val Val Thr Ala Pro
 490 495 500
 50 TAGGGCAGCC GGAGGAATG 1560

55 SEQ ID NO: 2
 Sequence length: 20

Sequence type: Nucleic acid
 Strandedness: Single
 Topology: Linear
 Molecular type: synthetic DNA
 Sequence
 GAGAATTCAT GCGGCAAAGC

20

SEQ ID NO: 3
 Sequence length: 16
 Sequence type: Nucleic acid
 Strandedness: Single
 Topology: Linear
 Molecular type: synthetic DNA
 Sequence
 GGGTCGACTA CCGTGC

16

SEQ ID NO: 4
 Sequence length: 1560
 Sequence type: Nucleic acid
 Strandedness: Double
 Topology: Linear
 Molecular type: cDNA

Sequence
 GAATTCGTGG CCCGCAGGGT TCCTCCAAG ATG GCG GCG CAG AGG AGG AGC TTG 53
 Met Ala Ala Gln Arg Arg Ser Leu
 5
 CTG CAG AGT GAG CAG CAG CCA AGC TGG ACA GAT GAC CTG CCT CTC TGC 101
 Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys
 10 15 20
 CAC CTC TCT GGG GTT GGC TCA GCC TCC AAC CGC AGC TAC TCT GCT GAT 149
 His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp
 25 30 35 40
 GGC AAG GGC ACT GAG AGC CAC CCG CCA GAG GAC AGA TGG CTC AAG TTC 197
 Gly Lys Gly Thr Glu Ser His Pro Pro Glu Asp Arg Trp Leu Lys Phe
 45 50 55

EP 0 803 571 A2

	AGG AGT GAG AAC AAC TGC TTC CTG TAT GGG GTC TTC AAC GGC TAT GAT	245
5	Arg Ser Glu Asn Asn Cys Phe Leu Tyr Gly Val Phe Asn Gly Tyr Asp	
	60 65 70	
	GGC AAC CGA GTG ACC AAC TTC GTG GCC CAG CGG CTG TCC GCA GAG CTC	293
	Gly Asn Arg Val Thr Asn Phe Val Ala Gln Arg Leu Ser Ala Glu Leu	
10	75 80 85	
	CTG CTG GGC CAG CTG AAT GCC GAG CAC GCC GAG GCC GAT GTG CGG CGT	341
	Leu Leu Gly Gln Leu Asn Ala Glu His Ala Glu Ala Asp Val Arg Arg	
15	90 95 100	
	GTG CTG CTG CAG GCC TTC GAT GTG GTG GAG AGG AGC TTC CTG GAG TCC	389
	Val Leu Leu Gln Ala Phe Asp Val Val Glu Arg Ser Phe Leu Glu Ser	
	105 110 115 120	
20	ATT GAC GAC GCC TTG GCT GAG AAG GCA AGC CTC CAG TCG CAA TTG CCA	437
	Ile Asp Asp Ala Leu Ala Glu Lys Ala Ser Leu Gln Ser Gln Leu Pro	
	125 130 135	
25	GAG GGA GTC CCT CAG CAC CAG CTG CCT CCT CAG TAT CAG AAG ATC CTT	485
	Glu Gly Val Pro Gln His Gln Leu Pro Pro Gln Tyr Gln Lys Ile Leu	
	140 145 150	
30	GAG AGA CTC AAG ACG TTA GAG AGG GAA ATT TCG GGA GGG GCC ATG GCC	533
	Glu Arg Leu Lys Thr Leu Glu Arg Glu Ile Ser Gly Gly Ala Met Ala	
	155 160 165	
35	GTT GTG GCG GTC CTT CTC AAC AAC AAG CTC TAC GTC GCC AAT GTC GGT	581
	Val Val Ala Val Leu Leu Asn Asn Lys Leu Tyr Val Ala Asn Val Gly	
	170 175 180	
40	ACA AAC CGT GCA CTT TTA TGC AAA TCG ACA GTG GAT GGG TTG CAG GTG	629
	Thr Asn Arg Ala Leu Leu Cys Lys Ser Thr Val Asp Gly Leu Gln Val	
	185 190 195 200	
	ACA CAG CTG AAC GTG GAC CAC ACC ACA GAG AAC GAG GAT GAG CTC TTC	677
45	Thr Gln Leu Asn Val Asp His Thr Thr Glu Asn Glu Asp Glu Leu Phe	
	205 210 215	
	CGT CTT TCG CAG CTG GGC TTG GAT GCT GGA AAG ATC AAG CAG GTG GGG	725
	Arg Leu Ser Gln Leu Gly Leu Asp Ala Gly Lys Ile Lys Gln Val Gly	
50	220 225 230	
	ATC ATC TGT GGG CAG GAG AGC ACC CGG CGG ATC GGG GAT TAC AAG GTT	773
	Ile Ile Cys Gly Gln Glu Ser Thr Arg Arg Ile Gly Asp Tyr Lys Val	
55	235 240 245	

EP 0 803 571 A2

AAA TAT GGC TAC ACG GAC ATT GAC CTT CTC AGC GCT GCC AAG TCC AAA 821
 Lys Tyr Gly Tyr Thr Asp Ile Asp Leu Leu Ser Ala Ala Lys Ser Lys
 5 250 255 260
 CCA ATC ATC GCA GAG CCA GAA ATC CAT GGG GCA CAG CCG CTG GAT GGG 869
 Pro Ile Ile Ala Glu Pro Glu Ile His Gly Ala Gln Pro Leu Asp Gly
 265 270 275 280
 10 GTG ACG GGC TTC TTG CTG CTG ATG TCG GAG GGG TTG TAC AAG GCC CTA 917
 Val Thr Gly Phe Leu Val Leu Met Ser Glu Gly Leu Tyr Lys Ala Leu
 285 290 295
 15 GAG GCA GCC CAT GGG CCT GGG CAG GCC AAC CAG GAG ATT GCT GCG ATG 965
 Glu Ala Ala His Gly Pro Gly Gln Ala Asn Gln Glu Ile Ala Ala Met
 300 305 310
 20 ATT GAC ACT GAG TTT GCC AAG CAG ACC TCC CTG GAC GCA GTG GCC CAG 1013
 Ile Asp Thr Glu Phe Ala Lys Gln Thr Ser Leu Asp Ala Val Ala Gln
 315 320 325
 GCC GTC GTG GAC CGG GTG AAG CGC ATC CAC AGC GAC ACC TTC GCC AGT 1061
 25 Ala Val Val Asp Arg Val Lys Arg Ile His Ser Asp Thr Phe Ala Ser
 330 335 340
 GGT GGG GAG CGT GCC AGG TTC TGC CCC CGG CAC GAG GAC ATG ACC CTG 1109
 30 Gly Gly Glu Arg Ala Arg Phe Cys Pro Arg His Glu Asp Met Thr Leu
 345 350 355 360
 CTA GTG AGG AAC TTT GGC TAC CCG CTG GGC GAA ATG AGC CAG CCC ACA 1157
 Leu Val Arg Asn Phe Gly Tyr Pro Leu Gly Glu Met Ser Gln Pro Thr
 35 365 370 375
 CCG AGC CCA GCC CCA GCT GCA GGA GGA CGA GTG TAC CCT GTG TCT GTG 1205
 Pro Ser Pro Ala Pro Ala Ala Gly Gly Arg Val Tyr Pro Val Ser Val
 380 385 390
 40 CCA TAC TCC AGC GCC CAG AGC ACC AGC AAG ACC AGC GTG ACC CTC TCC 1253
 Pro Tyr Ser Ser Ala Gln Ser Thr Ser Lys Thr Ser Val Thr Leu Ser
 395 400 405
 45 CTT GTC ATG CCC TCC CAG GGC CAG ATG GTC AAC GGG GCT CAC AGT GCT 1301
 Leu Val Met Pro Ser Gln Gly Gln Met Val Asn Gly Ala His Ser Ala
 410 415 420
 50 TCC ACC CTG GAC GAA GCC ACC CGC ACC CTC ACC AAC CAA AGC CCG ACC 1349
 Ser Thr Leu Asp Glu Ala Thr Pro Thr Leu Thr Asn Gln Ser Pro Thr
 425 430 435 440
 55

EP 0 803 571 A2

5 TTA ACC CTG CAG TCC ACC AAC ACG CAC ACG CAG AGC AGC AGC TCC AGC 1397
 Leu Thr Leu Gln Ser Thr Asn Thr His Thr Gln Ser Ser Ser Ser Ser
 445 450 455
 10 TCT GAC GGA GGC CTC TTC CGC TCC CGG CCC GCC CAC TCG CTC CCG CCT 1445
 Ser Asp Gly Gly Leu Phe Arg Ser Arg Pro Ala His Ser Leu Pro Pro
 460 465 470
 15 GGC GAG GAC GGT CGT GTT GAG CCC TAT GTG GAC TTT GCT GAG TTT TAC 1493
 Gly Glu Asp Gly Arg Val Glu Pro Tyr Val Asp Phe Ala Glu Phe Tyr
 475 480 485
 20 CGC CTC TGG AGC GTG GAC CAT GGC GAG CAG AGC GTG GTG ACA GCA CCG 1541
 Arg Leu Trp Ser Val Asp His Gly Glu Gln Ser Val Val Thr Ala Pro
 490 495 500
 TAGGGCAGCC GGAGGAATG 1560

25

30

35

40

45

50

55

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: NAOTO UENO
 (B) STREET: HOKKO KOKUMIN-SHUKUSHA # 1-101, HIGASHI 3 CHOME, KITA 26
 (C) CITY: HIGASHI-KU, SAPPORO-SHI
 (D) STATE: HOKKAIDO
 (E) COUNTRY: JP
 (F) POSTAL CODE (ZIP): NONE

(ii) TITLE OF INVENTION: TAB1 PROTEIN AND DNA CODING THEREFOR

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 97302808.7

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 126282/96
 (B) FILING DATE: 24-APR-1996

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: JP 300856/96
 (B) FILING DATE: 28-OCT-1996

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/752891
 (B) FILING DATE: 20-NOV-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

40 GAATTCGTGG CCCGACGGGT TCCTCCAAG ATG GCG GCG CAG AGG AGG AGC TTG 53
    Met Ala Ala Gln Arg Arg Ser Leu
    5
    CTG CAG AGT GAG CAG CAG CCA AGC TGG ACA GAT GAC CTG CCT CTC TGC 101
    Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys
    10      15      20
    CAC CTC TCT GGG GTT GGC TCA GCC TCC AAC CGC AGC TAC TCT GCT GAT 149
    His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp
    25      30      35      40
    GGC AAG GGC ACT GAG AGC CAC CCG CCA GAG GAC AGC TGG CTC AAG TTC 197
    Gly Lys Gly Thr Glu Ser His Pro Pro Glu Asp Ser Trp Leu Lys Phe
    45      50      55
    AGG AGT GAG AAC AAC TGC TTC CTG TAT GGG GTC TTC AAC GGC TAT GAT 245
    Arg Ser Glu Asn Asn Cys Phe Leu Tyr Gly Val Phe Asn Gly Tyr Asp
    60      65      70
    GGC AAC CGA GTG ACC AAC TTC GTG GCC CAG CGG CTG TCC GCA GAG CTC 293
    Gly Asn Arg Val Thr Asn Phe Val Ala Gln Arg Leu Ser Ala Glu Leu
    75      80      85

```

EP 0 803 571 A2

	CTG	CTG	GGC	CAG	CTG	AAT	GCC	GAG	CAC	GCC	GAG	GCC	GAT	GTG	CGG	CGT	341
	Leu	Leu	Gly	Gln	Leu	Asn	Ala	Glu	His	Ala	Glu	Ala	Asp	Val	Arg	Arg	
		90					95					100					
5	GTG	CTG	CTG	CAG	GCC	TTC	GAT	GTG	GTG	GAG	AGG	AGC	TTC	CTG	GAG	TCC	389
	Val	Leu	Leu	Gln	Ala	Phe	Asp	Val	Val	Glu	Arg	Ser	Phe	Leu	Glu	Ser	
	105					110					115					120	
	ATT	GAC	GAC	GCC	TTG	GCT	GAG	AAG	GCA	AGC	CTC	CAG	TCG	CAA	TTG	CCA	437
	Ile	Asp	Asp	Ala	Leu	Ala	Glu	Lys	Ala	Ser	Leu	Gln	Ser	Gln	Leu	Pro	
					125						130					135	
10	GAG	GGA	GTC	CCT	CAG	CAC	CAG	CTG	CCT	CAG	TAT	CAG	AAG	ATC	CTT		485
	Glu	Gly	Val	Pro	Gln	His	Gln	Leu	Pro	Pro	Gln	Tyr	Gln	Lys	Ile	Leu	
				140					145					150			
	GAG	AGA	CTC	AAG	ACG	TTA	GAG	AGG	GAA	ATT	TCG	GGA	GGG	GCC	ATG	GCC	533
	Glu	Arg	Leu	Lys	Thr	Leu	Glu	Arg	Glu	Ile	Ser	Gly	Gly	Ala	Met	Ala	
				155				160					165				
15	GTT	GTG	GCG	GTC	CTT	CTC	AAC	AAC	AAG	CTC	TAC	GTC	GCC	AAT	GTC	GGT	581
	Val	Val	Ala	Val	Leu	Leu	Asn	Asn	Lys	Leu	Tyr	Val	Ala	Asn	Val	Gly	
		170					175					180					
	ACA	AAC	CGT	GCA	CTT	TTA	TGC	AAA	TCG	ACA	GTG	GAT	GGG	TTG	CAG	GTG	629
	Thr	Asn	Arg	Ala	Leu	Leu	Cys	Lys	Ser	Thr	Val	Asp	Gly	Leu	Gln	Val	
		185				190					195					200	
20	ACA	CAG	CTG	AAC	GTG	GAC	CAC	ACC	ACA	GAG	AAC	GAG	GAT	GAG	CTC	TTC	677
	Thr	Gln	Leu	Asn	Val	Asp	His	Thr	Thr	Glu	Asn	Glu	Asp	Glu	Leu	Phe	
					205					210				215			
	CGT	CTT	TCG	CAG	CTG	GGC	TTG	GAT	GCT	GGA	AAG	ATC	AAG	CAG	GTG	GGG	725
	Arg	Leu	Ser	Gln	Leu	Gly	Leu	Asp	Ala	Gly	Lys	Ile	Lys	Gln	Val	Gly	
				220				225					230				
25	ATC	ATC	TGT	GGG	CAG	GAG	AGC	ACC	CGG	CGG	ATC	GGG	GAT	TAC	AAG	GTT	773
	Ile	Ile	Cys	Gly	Gln	Glu	Ser	Thr	Arg	Arg	Ile	Gly	Asp	Tyr	Lys	Val	
			235					240					245				
	AAA	TAT	GGC	TAC	ACG	GAC	ATT	GAC	CTT	CTC	AGC	GCT	GCC	AAG	TCC	AAA	821
	Lys	Tyr	Gly	Tyr	Thr	Asp	Ile	Asp	Leu	Leu	Ser	Ala	Ala	Lys	Ser	Lys	
		250				255						260					
30	CCA	ATC	ATC	GCA	GAG	CCA	GAA	ATC	CAT	GGG	GCA	CAG	CCG	CTG	GAT	GGG	869
	Pro	Ile	Ile	Ala	Glu	Pro	Glu	Ile	His	Gly	Ala	Gln	Pro	Leu	Asp	Gly	
		265				270					275					280	
	GTG	ACG	GGC	TTC	TTG	GTG	CTG	ATG	TCG	GAG	GGG	TTG	TAC	AAG	GCC	CTA	917
	Val	Thr	Gly	Phe	Leu	Val	Leu	Met	Ser	Glu	Gly	Leu	Tyr	Lys	Ala	Leu	
				285						290				295			
35	3AG	GCA	GCC	CAT	GGG	CCT	GGG	CAG	GCC	AAC	CAG	GAG	ATT	GCT	GCG	ATG	965
	Glu	Ala	Ala	His	Gly	Pro	Gly	Gln	Ala	Asn	Gln	Glu	Ile	Ala	Ala	Met	
				300					305					310			
	ATT	GAC	ACT	GAG	TTT	GCC	AAG	CAG	ACC	TCC	CTG	GAC	GCA	GTG	GCC	CAG	1013
	Ile	Asp	Thr	Glu	Phe	Ala	Lys	Gln	Thr	Ser	Leu	Asp	Ala	Val	Ala	Gln	
				315				320					325				
40	3CC	GTC	GTG	GAC	CGG	GTG	AAG	CGC	ATC	CAC	AGC	GAC	ACC	TTC	GCC	AGT	1061
	Ala	Val	Val	Asp	Arg	Val	Lys	Arg	Ile	His	Ser	Asp	Thr	Phe	Ala	Ser	
				330			335					340-					
	3GT	GGG	GAG	CGT	GCC	AGG	TTC	TGC	CCC	CGG	CAC	GAG	GAC	ATG	ACC	CTG	1109
	Gly	Gly	Glu	Arg	Ala	Arg	Phe	Cys	Pro	Arg	His	Glu	Asp	Met	Thr	Leu	
		345				350					355					360	
45	CTA	GTG	AGG	AAC	TTT	GGC	TAC	CCG	CTG	GGC	GAA	ATG	AGC	CAG	CCC	ACA	1157
	Leu	Val	Arg	Asn	Phe	Gly	Tyr	Pro	Leu	Gly	Glu	Met	Ser	Gln	Pro	Thr	
					365					370				375			
	CCG	AGC	CCA	GCC	CCA	GCT	GCA	GGA	GGA	CGA	GTG	TAC	CCT	GTG	TCT	GTG	1205
	Pro	Ser	Pro	Ala	Pro	Ala	Ala	Gly	Gly	Arg	Val	Tyr	Pro	Val	Ser	Val	
				380					385					390			
50	CCA	TAC	TCC	AGC	GCC	CAG	AGC	ACC	AGC	AAG	ACC	AGC	GTG	ACC	CTC	TCC	1253
	Pro	Tyr	Ser	Ser	Ala	Gln	Ser	Thr	Ser	Lys	Thr	Ser	Val	Thr	Leu	Ser	
				395				400					405				
	CTT	GTC	ATG	CCC	TCC	CAG	GGC	CAG	ATG	GTC	AAC	GGG	GCT	CAC	AGT	GCT	1301
	Leu	Val	Met	Pro	Ser	Gln	Gly	Gln	Met	Val	Asn	Gly	Ala	His	Ser	Ala	
				410			415					420					
55	TCC	ACC	CTG	GAC	GAA	GCC	ACC	CCC	ACC	CTC	ACC	AAC	CAA	AGC	CCG	ACC	1349

EP 0 803 571 A2

Ser Thr Leu Asp Glu Ala Thr Pro Thr Leu Thr Asn Gln Ser Pro Thr
 425 430 435 440
 TTA ACC CTG CAG TCC ACC AAC ACG CAC ACG CAG AGC AGC AGC TCC AGC 1397
 Leu Thr Leu Gln Ser Thr Asn Thr His Thr Gln Ser Ser Ser Ser Ser
 445 450 455
 TCT GAC GGA GGC CTC TTC CGC TCC CGG CCC GCC CAC TCG CTC CCG CCT 1445
 Ser Asp Gly Gly Leu Phe Arg Ser Arg Pro Ala His Ser Leu Pro Pro
 460 465 470
 GGC GAG GAC GGT CGT GTT GAG CCC TAT GTG GAC TTT GCT GAG TTT TAC 1493
 Gly Glu Asp Gly Arg Val Glu Pro Tyr Val Asp Phe Ala Glu Phe Tyr
 475 480 485
 CGC CTC TGG AGC GTG GAC CAT GGC GAG CAG AGC GTG GTG ACA GCA CCG 1541
 Arg Leu Trp Ser Val Asp His Gly Glu Gln Ser Val Val Thr Ala Pro
 490 495 500
 TAGGGCAGCC GGAGGAATG 1560

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAGAATTCAT GCGGCAAAGC

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid (synthetic DNA)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTCGACTA CGGTGC

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGTGG CCCGCAGGGT TCCTCCAAG ATG GCG GCG CAG AGG AGG AGC TTG 53
 Met Ala Ala Gln Arg Arg Ser Leu
 5
 CTG CAG AGT GAG CAG CAG CCA AGC TGG ACA GAT GAC CTG CCT CTC TGC 101
 Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys
 10 15 20
 CAC CTC TCT GGG GTT GGC TCA GCC TCC AAC CGC AGC TAC TCT GCT GAT 149
 His Leu Ser Gly Val Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp
 25 30 35 40
 GGC AAG GGC ACT GAG AGC CAC CCG CCA GAG GAC AGA TGG CTC AAG TTC 197
 Gly Lys Gly Thr Glu Ser His Pro Pro Glu Asp Arg Trp Leu Lys Phe

EP 0 803 571 A2

				45					50					55					
	AGG	AGT	GAG	AAC	AAC	TGC	TTC	CTG	TAT	GGG	GTC	TTC	AAC	GGC	TAT	GAT		245	
	Arg	Ser	Glu	Asn	Asn	Cys	Phe	Leu	Tyr	Gly	Val	Phe	Asn	Gly	Tyr	Asp			
				60					65					70					
5	GGC	AAC	CGA	GTG	ACC	AAC	TTC	GTG	GCC	CAG	CGG	CTG	TCC	GCA	GAG	CTC		293	
	Gly	Asn	Arg	Val	Thr	Asn	Phe	Val	Ala	Gln	Arg	Leu	Ser	Ala	Glu	Leu			
				75				80						85					
	CTG	CTG	GGC	CAG	CTG	AAT	GCC	GAG	CAC	GCC	GAG	GCC	GAT	GTG	CGG	CGT		341	
	Leu	Leu	Gly	Gln	Leu	Asn	Ala	Glu	His	Ala	Glu	Ala	Asp	Val	Arg	Arg			
				90				95						100					
10	GTG	CTG	CTG	CAG	GCC	TTC	GAT	GTG	GTG	GAG	AGG	AGC	TTC	CTG	GAG	TCC		389	
	Val	Leu	Leu	Gln	Ala	Phe	Asp	Val	Val	Glu	Arg	Ser	Phe	Leu	Glu	Ser			
				105				110						115				120	
	ATT	GAC	GAC	GCC	TTG	GCT	GAG	AAG	GCA	AGC	CTC	CAG	TCG	CAA	TTG	CCA		437	
	Ile	Asp	Asp	Ala	Leu	Ala	Glu	Lys	Ala	Ser	Leu	Gln	Ser	Gln	Leu	Pro			
				125										130					
15	GAG	GGA	GTC	CCT	CAG	CAC	CAG	CTG	CCT	CCT	CAG	TAT	CAG	AAG	ATC	CTT		485	
	Glu	Gly	Val	Pro	Gln	His	Gln	Leu	Pro	Pro	Gln	Tyr	Gln	Lys	Ile	Leu			
				140										150					
	GAG	AGA	CTC	AAG	ACG	TTA	GAG	AGG	GAA	ATT	TCG	GGA	GGG	GCC	ATG	GCC		533	
	Glu	Arg	Leu	Lys	Thr	Leu	Glu	Arg	Glu	Ile	Ser	Gly	Gly	Ala	Met	Ala			
				155										165					
20	GTT	GTG	GCG	GTC	CTT	CTC	AAC	AAC	AAG	CTC	TAC	GTC	GCC	AAT	GTC	GGT		581	
	Val	Val	Ala	Val	Leu	Leu	Asn	Asn	Lys	Leu	Tyr	Val	Ala	Asn	Val	Gly			
				170										180					
	ACA	AAC	CGT	GCA	CTT	TTA	TGC	AAA	TCG	ACA	GTG	GAT	GGG	TTG	CAG	GTG		629	
	Thr	Asn	Arg	Ala	Leu	Leu	Cys	Lys	Ser	Thr	Val	Asp	Gly	Leu	Gln	Val			
				185										195				200	
25	ACA	CAG	CTG	AAC	GTG	GAC	CAC	ACC	ACA	GAG	AAC	GAG	GAT	GAG	CTC	TTC		677	
	Thr	Gln	Leu	Asn	Val	Asp	His	Thr	Thr	Glu	Asn	Glu	Asp	Glu	Leu	Phe			
				205										215					
	CGT	CTT	TCG	CAG	CTG	GGC	TTG	GAT	GCT	GGA	AAG	ATC	AAG	CAG	GTG	GGG		725	
	Arg	Leu	Ser	Gln	Leu	Gly	Leu	Asp	Ala	Gly	Lys	Ile	Lys	Gln	Val	Gly			
				220										230					
30	ATC	ATC	TGT	GGG	CAG	GAG	AGC	ACC	CGG	CGG	ATC	GGG	GAT	TAC	AAG	GTT		773	
	Ile	Ile	Cys	Gly	Gln	Glu	Ser	Thr	Arg	Arg	Ile	Gly	Asp	Tyr	Lys	Val			
				235										245					
	AAA	TAT	GGC	TAC	ACG	GAC	ATT	GAC	CTT	CTC	AGC	GCT	GCC	AAG	TCC	AAA		821	
	Lys	Tyr	Gly	Tyr	Thr	Asp	Ile	Asp	Leu	Leu	Ser	Ala	Ala	Lys	Ser	Lys			
				250										260					
35	CCA	ATC	ATC	GCA	GAG	CCA	GAA	ATC	CAT	GGG	GCA	CAG	CCG	CTG	GAT	GGG		869	
	Pro	Ile	Ile	Ala	Glu	Pro	Glu	Ile	His	Gly	Ala	Gln	Pro	Leu	Asp	Gly			
				265										275				280	
	GTG	ACG	GGC	TTC	TTG	GTG	CTG	ATG	TCG	GAG	GGG	TTG	TAC	AAG	GCC	CTA		917	
	Val	Thr	Gly	Phe	Leu	Val	Leu	Met	Ser	Glu	Gly	Leu	Tyr	Lys	Ala	Leu			
				285										295					
40	GAG	GCA	GCC	CAT	GGG	CCT	GGG	CAG	GCC	AAC	CAG	GAG	ATT	GCT	GCG	ATG		965	
	Glu	Ala	Ala	His	Gly	Pro	Gly	Gln	Ala	Asn	Gln	Glu	Ile	Ala	Ala	Met			
				300										310					
	ATT	GAC	ACT	GAG	TTT	GCC	AAG	CAG	ACC	TCC	CTG	GAC	GCA	GTG	GCC	CAG		1013	
	Ile	Asp	Thr	Glu	Phe	Ala	Lys	Gln	Thr	Ser	Leu	Asp	Ala	Val	Ala	Gln			
				315										325					
45	GCC	GTC	GTG	GAC	CGG	GTG	AAG	CGC	ATC	CAC	AGC	GAC	ACC	TTC	GCC	AGT		1061	
	Ala	Val	Val	Asp	Arg	Val	Lys	Arg	Ile	His	Ser	Asp	Thr	Phe	Ala	Ser			
				330										340					
	GGT	GGG	GAG	CGT	GCC	AGG	TTC	TGC	CCC	CGG	CAC	GAG	GAC	ATG	ACC	CTG		1109	
	Gly	Gly	Glu	Arg	Ala	Arg	Phe	Cys	Pro	Arg	His	Glu	Asp	Met	Thr	Leu			
				345										355				360	
50	CTA	GTG	AGG	AAC	TTT	GGC	TAC	CCG	CTG	GGC	GAA	ATG	AGC	CAG	CCC	ACA		1157	
	Leu	Val	Arg	Asn	Phe	Gly	Tyr	Pro	Leu	Gly	Glu	Met	Ser	Gln	Pro	Thr			
				365										375					
	CCG	AGC	CCA	GCC	CCA	GCT	GCA	GGA	GGA	CGA	GTG	TAC	CCT	GTG	TCT	GTG		1205	
	Pro	Ser	Pro	Ala	Pro	Ala	Ala	Gly	Gly	Arg	Val	Tyr	Pro	Val	Ser	Val			
				380										390					
55																			

EP 0 803 571 A2

	CCA	TAC	TCC	AGC	GCC	CAG	AGC	ACC	AGC	AAG	ACC	AGC	GTG	ACC	CTC	TCC	1253
	Pro	Tyr	Ser	Ser	Ala	Gln	Ser	Thr	Ser	Lys	Thr	Ser	Val	Thr	Leu	Ser	
			395					400					405				
5	CTT	GTC	ATG	CCC	TCC	CAG	GGC	CAG	ATG	GTC	AAC	GGG	GCT	CAC	AGT	GCT	1301
	Leu	Val	Met	Pro	Ser	Gln	Gly	Gln	Met	Val	Asn	Gly	Ala	His	Ser	Ala	
		410					415					420					
	TCC	ACC	CTG	GAC	GAA	GCC	ACC	CCC	ACC	CTC	ACC	AAC	CAA	AGC	CCG	ACC	1349
	Ser	Thr	Leu	Asp	Glu	Ala	Thr	Pro	Thr	Leu	Thr	Asn	Gln	Ser	Pro	Thr	
	425						430				435					440	
10	TTA	ACC	CTG	CAG	TCC	ACC	AAC	ACG	CAC	ACG	CAG	AGC	AGC	AGC	TCC	AGC	1397
	Leu	Thr	Leu	Gln	Ser	Thr	Asn	Thr	His	Thr	Gln	Ser	Ser	Ser	Ser	Ser	
					445				450						455		
	TCT	GAC	GGA	GGC	CTC	TTC	CGC	TCC	CGG	CCC	CAC	TCG	CTC	CCG	CCT	1445	
	Ser	Asp	Gly	Gly	Leu	Phe	Arg	Ser	Arg	Pro	Ala	His	Ser	Leu	Pro	Pro	
15				460				465				470					
	GGC	GAG	GAC	GGT	CGT	GTT	GAG	CCC	TAT	GTG	GAC	TTT	GCT	GAG	TTT	TAC	1493
	Gly	Glu	Asp	Gly	Arg	Val	Glu	Pro	Tyr	Val	Asp	Phe	Ala	Glu	Phe	Tyr	
			475					480				485					
	CGC	CTC	TGG	AGC	GTG	GAC	CAT	GGC	GAG	CAG	AGC	GTG	GTG	ACA	GCA	CCG	1541
20	Arg	Leu	Trp	Ser	Val	Asp	His	Gly	Glu	Gln	Ser	Val	Val	Thr	Ala	Pro	
		490					495					500					
	TAGGGCAGCC GGAGGAATG																1560

25 Claims

1. An isolated DNA coding for TAB1 protein having the amino acid sequence shown in SEQ ID NO: 1.
2. An isolated DNA coding for protein having an amino acid sequence modified by a substitution, deletion and/or addition of one or more amino acids in the amino acid sequence shown in SEQ ID NO: 1, and having a biological property of TAB1 protein.
3. A DNA which can hybridize with DNA having the nucleotide sequence shown in SEQ ID NO: 1 under hybridization conditions of 60°C, 0.1 x SSC, 0.1% sodium dodecyl sulfate, and which has a biological property of TAB1 protein.
4. An isolated DNA coding for a protein having an amino acid sequence consisting of the amino acids from amino acid positions 21 to 579 of the amino acid sequence shown in SEQ ID NO: 1.
5. An isolated DNA coding for a polypeptide having the amino acid sequence consisting of the 68 amino acids from amino acid positions 437 to 504 of the amino acid sequence shown in SEQ ID NO: 1.
6. An isolated DNA according to claimed in claim 2, wherein the 52nd amino acid in the amino acid sequence shown in SEQ ID NO: 1 is arginine.
7. A DNA coding for a fusion protein comprising a protein or polypeptide according to any of claims 1 to 6.
8. A method for producing a protein or polypeptide comprising the steps of:

culturing a host transformed by an expression vector comprising DNA according to any one of claims 1 to 7, and recovering said protein or polypeptide from the culture.
9. A method according to claim 8, wherein said host is a mammalian cell or yeast cell.
10. A method for inducing mammalian cells to produce a protein or polypeptide according to any of claims 1 to 7, comprising the step of introducing DNA encoding said protein or polypeptide into mammalian cells.
11. An expression vector comprising DNA according to any one of claims 1 to 7.

EP 0 803 571 A2

12. A host transformed by an expression vector according to claim 11.

13. A host according to claim 12, wherein said host is a mammalian cell or yeast cell.

5 14. A method for screening TGF- β signaling pathway inhibitors, characterized by (A) contacting a sample containing TGF- β signaling pathway inhibitors with or introducing it into cells expressing a TAB1 protein or polypeptide encoded DNA according to any of claims 1 to 6 and TAK1 protein, and (B) measuring the kinase activity of the TAK1 protein.

10

15

20

25

30

35

40

45

50

55

Fig.1

GAD-TAB1

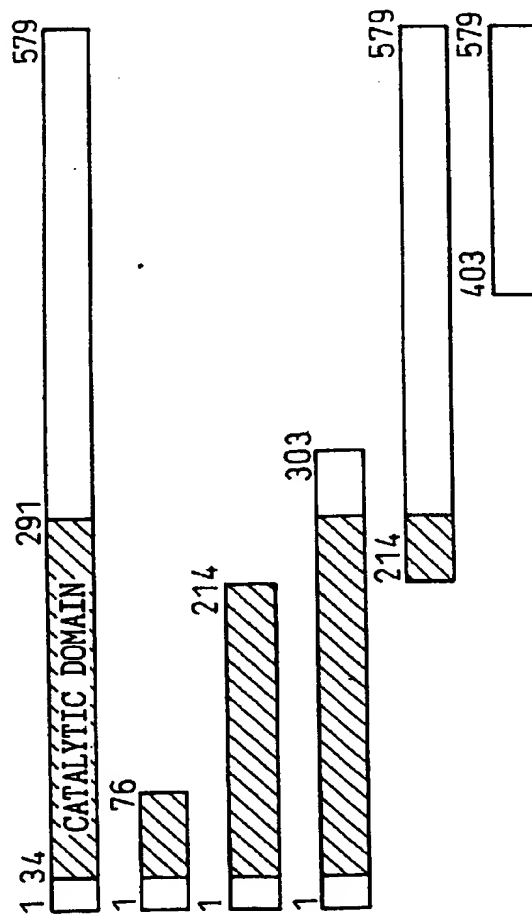


Fig.2

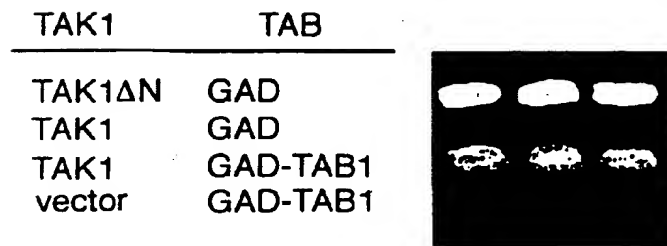


Fig.3

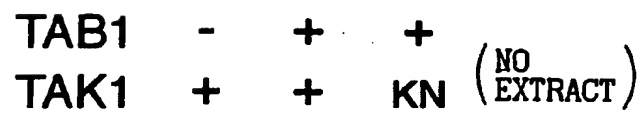


Fig.5

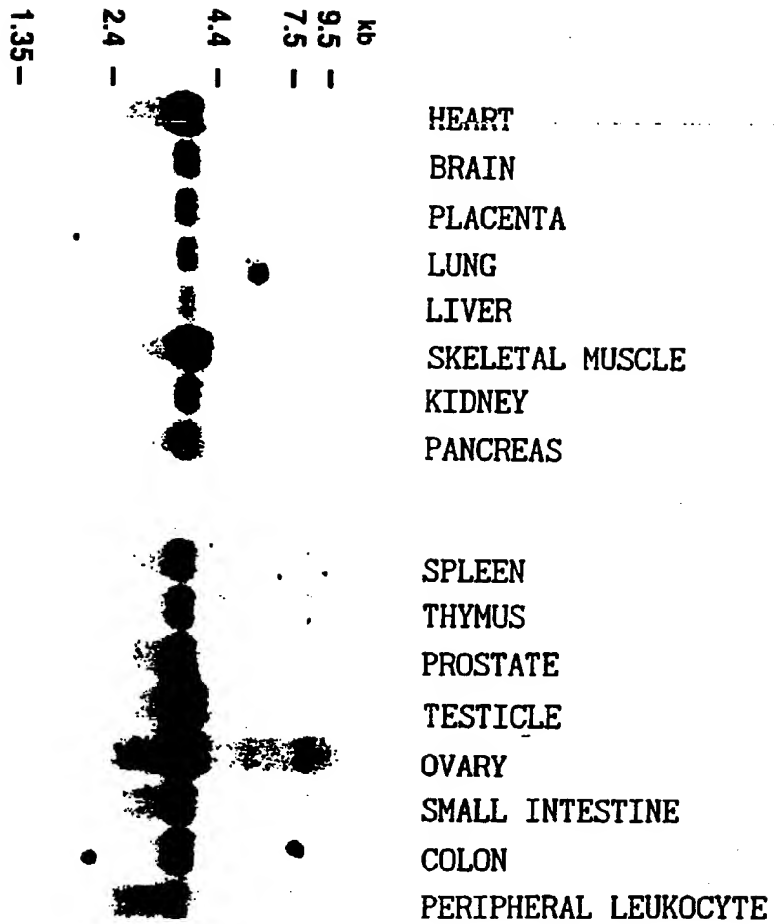


Fig.4

MAAQRRLQSEQQPSWIDDLPLCHLSGVGSASNRYSADGKGIESHPEDSWLKFRSEN	60
NCFLYGVFNQYDGNRVTNFVAQRLSAELLGQLNAEHAEDVRRVLLQAFDVVERSFLES	120
IDDALAEKASLSQLPEGVPQHQLPPQYQKILERLKTLEREISGGAMAVVAVLLNNKLYV	180
ANVGTNRALLCKSTVDGLQVTQLNVDHATTENEDELFRLSQLGLDAGKIKQVGIICQUEST	240
RRIGDYKVYGYTDIDLLSAAKSKPIIAEPEIHGAQPLDGVGTGLVLMSEGLYKALEAAH	300
GPGQANQEIAAMIDTEFAKQTSLDAVAQAVVDRVKRIHSDTFASGGERARFCPRHEDMTL	360
LVRNFGYPLGEMSQPTPSPAPAAAGRVYPVSVPYSSAQSTSKTSVTLVMPSPQGMVNG	420
AHSASTLDEATPTLTNQSP TLTLQSTNTHTQSSSSSSDGGLRFRSRPAHSLPPGEDGRVEP	480

** . . . ***** . . .

TAK1	1	MSTASAASSSSSSSSASEMIEAPSQ	
------	---	---------------------------	--

YVDFAEFYRLWSVDHGEQSVVTAP

504

Fig.6

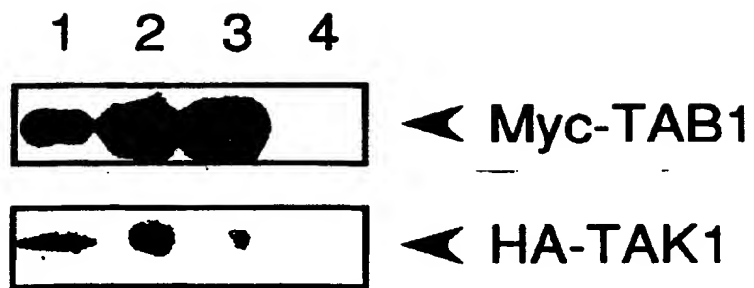


Fig. 8

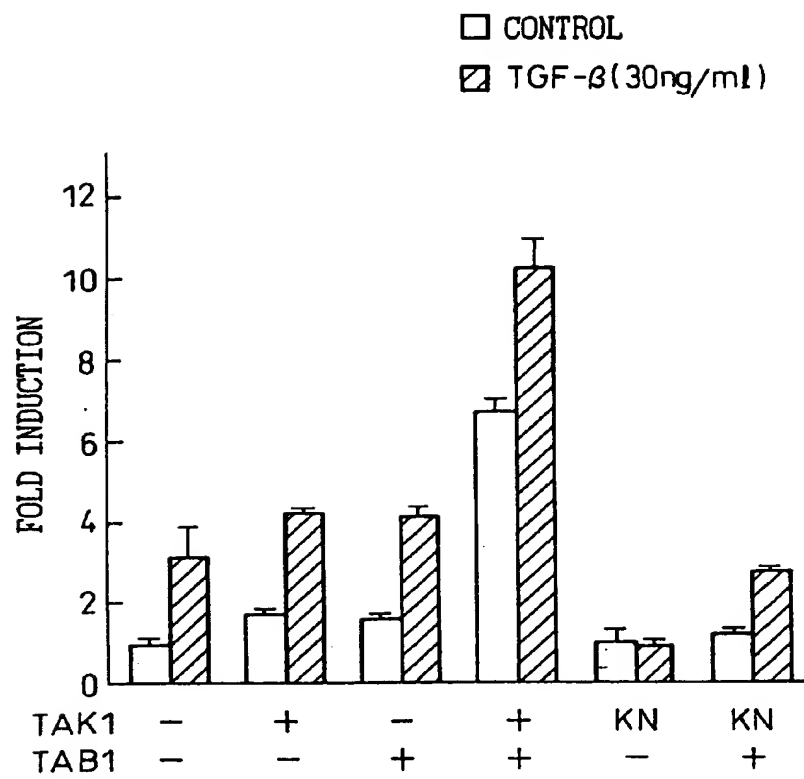


Fig.7

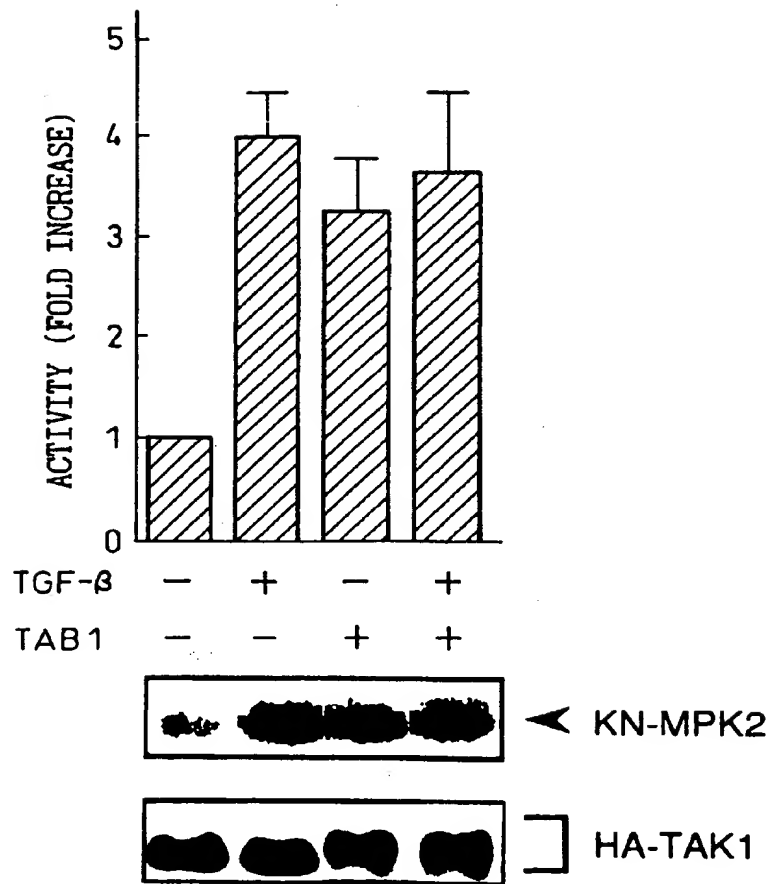
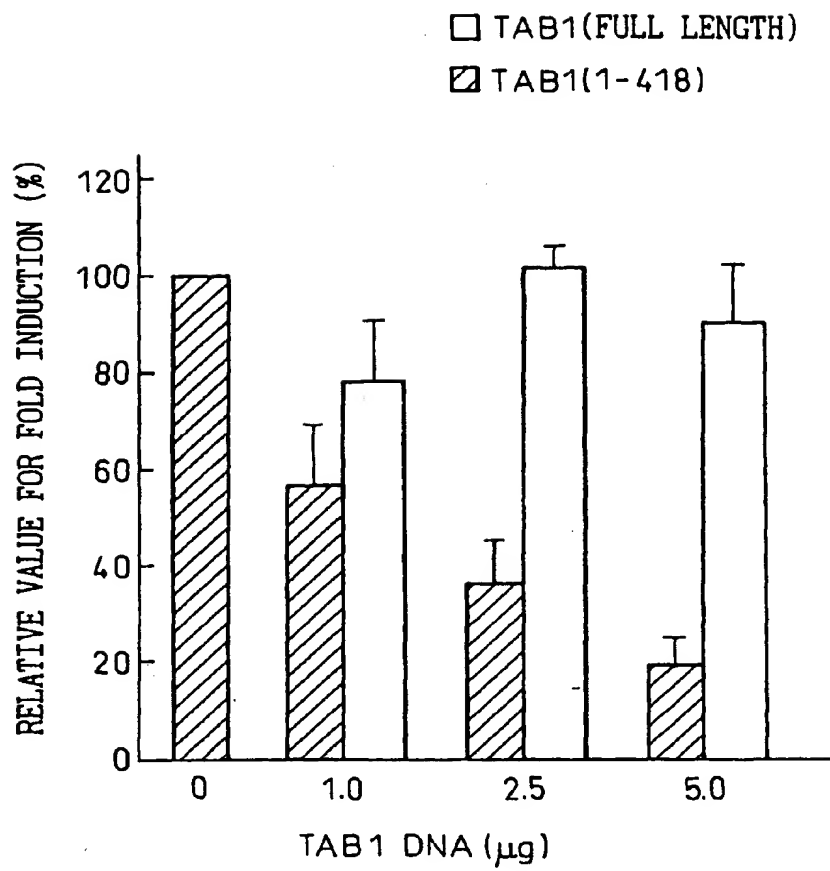


Fig.9



(19)



Europäisches Patentamt
European Patent Office
Office européen des brevets



(11)

EP 0 803 571 A3

(12)

EUROPEAN PATENT APPLICATION

(88) Date of publication A3:
28.07.1999 Bulletin 1999/30

(51) Int Cl.⁶: **C12N 15/12, C12N 15/62,**
C12Q 1/48

(43) Date of publication A2:
29.10.1997 Bulletin 1997/44

(21) Application number: **97302808.7**

(22) Date of filing: **24.04.1997**

(84) Designated Contracting States:
AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC
NL PT SE

(30) Priority: **24.04.1996 JP 12628296**
28.10.1996 JP 30085696
20.11.1996 US 752891

(71) Applicant: **CHUGAI SEIYAKU KABUSHIKI**
KAISHA
Tokyo 115 (JP)

(72) Inventors:
• **Matsumoto, Kunihiro**
Chikusa-ku, Nagoya-shi, Aichi (JP)
• **Nishida, Eisuke, Pakuhaimu Takaragake 610**
Sakyo-ku, Kyoto-shi, Kyoto (JP)

(74) Representative: **Wakerley, Helen Rachael**
Reddie & Grose,
16 Theobalds Road
London WC1X 8PL (GB)

(54) **Tab1 protein & dna coding therefor**

(57) DNA coding for TAB1 protein having activity
which activates factor TAK1 in the TGF- β signaling path-

way, and having the amino acid sequence shown in Seq.
ID. NO:1.

EP 0 803 571 A3

EP 0 803 571 A3



European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 97 30 2808

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
P,X	SHIBUYA, H. ET AL.: "TAB1: An Activator of the TAK1 MAPKKK in TGF-beta Signal Transduction" SCIENCE, vol. 272, 24 May 1996, pages 1179-1182, XP002103398 * the whole document *	1-14	C12N15/12 C12N15/62 C12Q1/48
D,A	YAMAGUCHI, K. ET AL.: "Identification of a Member of the MAPKKK Family as a Potential Mediator of TGF-beta Signal Transduction" SCIENCE, vol. 270, 22 December 1995, pages 2008-2011, XP002103399 * the whole document *	1-14	
			TECHNICAL FIELDS SEARCHED (Int.Cl.6)
			C07K C12N C12Q
The present search report has been drawn up for all claims			
Place of search BERLIN		Date of completion of the search 31 May 1999	Examiner Fuchs, U
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

EPF FORM 1503 03 EP (P04C01)